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FIGURE 1-1

FIGURE 1-1 **FIGURE 1-2** **FIGURE 1-3** **FIGURE 1-4** **FIGURE 1-5**

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FIGURE 1-2

220		240		260	
72	K A N V T N L L I A N L A F S D F L M C			91	331
280		300		320	
92	L L C Q P L T A V Y T I M D Y W I F G E			111	391
340		360		380	
112	T L C K M S A F I Q C M S V T V S I L S			131	451
400		420		440	
132	L V L V A L E R H Q L I I N P T G W K P			151	511
460		480		500	
152	S I S Q A Y L G I V L I W V I A C V L S			171	571

272 AAGCCAACGTAACCTGCCAACTGGCTTATCGCTTATCCTGCCTCTGACTTCCTCATGTGC
 72 K A N V T N L L I A N L A F S D F L M C 91 331

332 CTCCCTGTGCCAGCCCCCTGACCCGGTCTACACCATCATGGACTACTGGATTCCTTGAGAG
 92 L L C Q P L T A V Y T I M D Y W I F G E 111 391

392 ACCCTCTGCCAAGATGTCGGCCTCATCCAGTCATGTCGGTGAAGGTCTCCATCCTCTCG
 112 T L C K M S A F I Q C M S V T V S I L S 131 451

452 CTCGTCTCGTGGCCCTGGAGAGGCATCAGCTCATCAACCCAACAGGCTGGAAAGCCC
 132 L V L V A L E R H Q L I I N P T G W K P 151 511

512 AGCATCTCACAGGGCTAACCTGGCATTTGGCTCATTCCTGCTCATTCCTCTCC
 152 S I S Q A Y L G I V L I W V I A C V L S 171 571

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FIGURE 1-3

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FIGURE 1-4

872	GTCGCCCTTGGCGCTCTGGCTGCATGTTCAACAGCCTGGAAAGACTGGCAC	931
272	V A F A V L W L P L H V F N S L E D W H	291
880	900	920
932	CATGAGGCCATCCCATCTGCCACCGGAACCTCATCTTCTTAGTGTGCCACTTGCTtGCC	991
292	H E A I P I C H G N L I F L V C H L L A	311
940	960	980
992	ATGGCCTCCACCTGGCTCAACCCATTCAATCTATGGCTTTCTCAACACCAACTTCAAGAAG	1051
312	M A S T C V N P F I Y G F L N T N F K K	331
1000	1020	1040
1052	GAGATCAAGGCCCTGGCTGACTTGCCAGGAGCCCCCTGGAGGAGTCGGAGCAT	1111
332	E I K A L V L T C Q S A P L E E S E H	351
1060	1080	1100
1112	CTGGCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAACAGTGGCAGG	1171
352	L P L S T V H T E V S K G S L R L S G R	371

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FIGURE 1-5

1120		1140	
1172	TCCAAATCCCATTAAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCTGCCAGGCCTCTTC	1160	
372	S N P I *		
1180			1231 375
1200		1220	
1232	CACTTAGCTAAGTGGCACACTGCAAGCTGGGTGGCACCCCCAGCATTCCCTGGCTTCTG		1291

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FIGURE 2-1

FIGURE 2-1
FIGURE 2-2
FIGURE 2-3

hp25a human Y1 rat Y1 mouse Y1	1 MNTSHILLALL LPKSPQGENR SKPLGTPYNF SEHCQDSVDV MVFIVTYSI MN .STLFSQV ENHSVHSNF ERNAQLLAFE NDDCHLPLAM IFTLALAYGA MN .STLFSRV ENYSVHYNVS E.NSPFLAFE NDDCHLPLAV IFTLALAYGA MN .STLFSKV ENHGIHYNAS E.NSPLLAFE NDDCHLPLAV IFTLALAYGA	50 51 I ETVGVLCGNL CLMCVTVROK EKANVTNLLT ANLAFAFDLML CLLCQPLTAV VILGVSGNL ALIIIIILKK EMRNVTNLLT VNLSPSDLLV AIMCLBPFTFV VILGVSGNL ALIIIIILKK EMRNVTNLLT VNLSFSDLLV AVMCLBPFTFV VILGVSGNL ALIIIIILKK EMRNVTNLLT VNLSFSDLLV AVMCLBPFTFV	100 101 III XTIMDYWIFG ETLCKMSAFI QCMSVTVSIL SLVIVALERH QLIINPTGWK YTLMDHWF G EAMCKLNPFV QCVSITVSIF SLVILIAVERH QLIINPRGWR YTLMDHWF G ETMCKLNPFV QCVSITVSIF SLVILIAVERH QLIINPRGWR YTLMDHWF G ETMCKLNPFV QCVSITVSIF SLVILIAVERH QLIINPRGWR	150 151 IV PSISQAYLGI VLIWVIACVL SLPFLANSIL ENVFKHNHSK ALEFLADKVV PNNRHAYVGI AVIWVLAVAS SLPFLIYQWM TDEPFQNVT .LDAYKDKVV PNNRHAYIGI TVIWVLAVAS SLPFVIYQIL TDEPFQNVS .LAAFKDKVV PNNRHAYIGI TVIWVLAVAS SLPFVIYQIL TDEPFQNVS .LAAFKDKVV	hp25a human Y1 rat Y1 mouse Y1
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FIGURE 2-2

hp25a human Y1 rat Y1 mouse Y1	201 CTESWPLAHH RIVYTTFILL P0YCLPIGFI LVCYARIYRR LQRQGRVFRK CFDQFPSSDH RLSYTTLVV LQYFGPLCFI FICYFKIYIR LKRRNNMDK CFDKFPSSDH RLSYTTLVV LQYFGPLCPI FICYFKIYIR LKRRNNMDK CFDKFPSSDH RLSYTTLVV LQYFGPLCPI FICYFKIYIR LKRRNNMDK
	250 V GTYS.LRAGH MKQVNWLWV MVVAFAVWL PLHVFNLED WHHEAIPICH MRDNKYRSSE TKRINIMLLS IVVAFAVCML PLTIFNTVFD WNHQIATCN IRDSKYRSSE TKRINIMLLS IVVAFAVCML PLTIFNTVFD WNHQIATCN IRDSKYRSSE TKRINIMLLS IVVAFAVCML PLTIFNTVFD WNHQIATCN
	301 VI GNLLFLVCHL LAMASTCVNP FIYGFLNTNP KKEIKALVLT CQQSAPLEES HNLLFLCHL TAMISTCVNP IFYGFLNKNF QRDLQFFPNF CDFRSRDDD HNLLFLCHL TAMISTCVNP IFYGFLNKNF QRDLQFFPNF CDFRSRDDD HNLLFLCHL TAMISTCVNP IFYGFLNKNF QRDLQFFPNF CDFRSRDDD
	350 VII GNLLFLVCHL LAMASTCVNP FIYGFLNTNP KKEIKALVLT CQQSAPLEES HNLLFLCHL TAMISTCVNP IFYGFLNKNF QRDLQFFPNF CDFRSRDDD HNLLFLCHL TAMISTCVNP IFYGFLNKNF QRDLQFFPNF CDFRSRDDD HNLLFLCHL TAMISTCVNP IFYGFLNKNF QRDLQFFPNF CDFRSRDDD

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FIGURE 2-3

351 EHLPLSTVHT EVSKGSLRLS GRSNPI*
 ETIAMSTWHT DVSKTSLKQA SPVAFKKINN NDDNEKI*
 ETIAMSTWHT DVSKTSLKQA SPVAFKKISM N.DNEKI*
 ETIAMSTWHT DVSKTSLKQA SPVAFKKISM N.DNEKV*

mouse Y1
rat Y1
human Y1
hp25a

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FIGURE 3-1

FIGURE 3-1
FIGURE 3-2
FIGURE 3-3
FIGURE 3-4

-170

-150

-130

ATAGCTCTCAAGCCATAAGATATAAGTAGCTAAGAATTGTCTCCCTCTCCCTGTCCCTTG

-110

-90

-70

TTCTTACCTGGTCCATTTACATGCCTGGACCTTGAGTTCCATTGTTGTTGCAG

-50

-30

-10

GCTACACTCAGAAGTGGGCCCTTAGTCTTGAAGTTCTGGTCTTCACACCCACCATG

M

10

30

50

AATAACCTCTCATCTCATGGCCTCCCTTCTCCGGCATTCTACAAGGTAAGAATGGGACC
N T S H L M A S L S P A F L Q G K N G T

70

90

110

AACCCACTGGATTCCCTCTATAATCTCTCTGACGGCTGCCAGGATTGGCAGATCTGTTG
N P L D S L Y N L S D G C Q D S A D L L

130

150

170

GCCTTCATCATCACCAACCTACAGCGTTGAGACCGTCTGGGGCTCTAGGAAACCTCTGC
A F I I T T Y S V E T V L G V L G N L C

190

210

230

TTGATATTGTGACCACAAGGAAAAGGAAATGTCCAATGTGACCAACCTACTCATTGCC
L I F V T T R Q K E K S N V T N L L I A

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FIGURE 3-2

250 270 290

AACCTGGCCTTCTCTGACTTCCTCATGTGTCTCATCTGCCAGCCGCTCACGGTCACCTAC
 N L A F S D F L M C L I C Q P L T V T Y

310 330 350

ACCATCATGGACTACTGGATCTCGGCAGTCCTTGCAAGATGTTAACGTTACATCCAG
 T I M D Y W I F G E V L C K M L T F I Q

370 390 410

TGTATGTCGGTGACAGTCTCCATCCTCTCACTGGCCTTGTGGCCCTGGAGAGGCACCAAG
 C M S V T V S I L S L V L V A L E R H Q

430 450 470

CTCATTATCAACCCGACTGGCTGGAAACCCAGCATTTCCCAGGCCTACCTGGGGATTGTG
 L I I N P T G W K P S I S Q A Y L G I V

490 510 530

GTCATCTGGTCATTTCTTGTTCCTCTCCTGCCCTTCTGGCCAATAGCATCCTGAAC
 V I W F I S C F L S L P F L A N S I L N

550 570 590

GACCTCTCCACTACAACCACTCTAAGGTTGTGGAGTTCTGGAAGACAAGGTTGTCTGC
 D L F H Y N H S K V V E F L E D K V V C

610 630 650

TTTGTGTCTGGTCCTCGGATCACCAACCGCCTCATCTACACCACCTTCTGCTGCTCTC
 F V S W S S D H H R L I Y T T F L L L F

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FIGURE 3-3

670

690

710

CAATACTGCGTCCTCTGGCCTTCATCCTGGTCTGCTACATGCGTATCTATCAGCGCCTG
 Q Y C V P L A F I L V C Y M R I Y Q R L

730

750

770

CAGAGGCAGAGGCAGCGTTCCACACGCACACTTGCAGCTCACGAGTGGGCAGATGAAG
 Q R Q R R A F H T H T C S S R V G Q M K

790

810

830

CGGATCAATGGCATGCTCATGGCAATGGTACTGCCTTGAGTTCTCTGGCTGCCCTG
 R I N G M L M A M V T A F A V L W L P L

850

870

890

CATGTGTTAACACTCTGGAGGACTGGTACCAAGGAAGCCATCCCTGCTTGCATGGCAAC
 H V F N T L E D W Y Q E A I P A C H G N

910

930

950

CTCATCTTCTTGATGTGCCACCTGTTGCCATGGCTTCCACCTGTGTCAACCCTTCATC
 L I F L M C H L F A M A S T C V N P F I

970

990

1010

TATGGCTTCTAACATCAACTCAAGAAGGACATCAAGGCTCTGGTTCTGACCTGCCGT
 Y G F L N I N F K K D I K A L V L T C R

1030

1050

1070

TGCAGGCCACCTCAAGGGAGCCTGAGCCTCTGCCCTGTCCACTGTGCACACGGACCTC
 C R P P Q G E P E P L P L S T V H T D L

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1090

1110

1130

TCCAAGGGATCTATGAGGATGGGTAGCAAGTCTAACGTATGTAGTCATGTCTAGGCTCT
S K G S M R M G S K S N V M *

1150

1170

1190

TCCGCCATTTCCTTCGACACACCCCTTCACTGAGCTAAGTAGACACAATGCAAGCTGTG

1210

1230

1250

GTATCATCCTGCCATTCTGGTCTTGCGGCCAGACAGGCAGCAAGAGACTTGAAGCTT

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FIGURE 4

1

50

Y4rat MNTSHLMASL SPAFLQGKNG TNPLDSLYNL SDGCQDSADL LAFIITTYSV
 Y4hum MNTSHLLALL LPKSPQGENR SKPLGTPYNF SEHCQDSVDV MVFIVTSYSI

51

100

— I —

II

Y4rat ETVLGVLGNL CLIFVTTRQK EKSNVTNLLI ANLAFSDFLM CLICQPLTVT
 Y4hum ETVVGVLGNL CLMCVTVRQK EKANVTNLLI ANLAFSDFLM CLLCQPLTAV

101

150

— II —

III

Y4rat YTIMDYWIPG EVLCKMLTFI QCMSVTVSIL SLVLVALERH QLIINPTGWK
 Y4hum YTIMDYWIPG ETLCKMSAFI QCMSVTVSIL SLVLVALERH QLIINPTGWK

151

200

IV

Y4rat PSISQAYLGI VVIWFISCPL SLPFLANSIL NDLFHYNHSK VVEFLEDKV
 Y4hum PSISQAYLGI VLIWVIACVL SLPFLANSIL ENVPHKNHSK ALEFLADKV

201

250

V

Y4rat CFVSWSSDH~~H~~ RLIYTTFLLL PQYCVPLAFI LV CYM RIYQR LQRQRRAFH~~T~~
 Y4hum CTESWPLAH~~H~~ RTIYTTFLLL PQYCLPLGFI LV CYARIYRR LQRQGRVPH~~K~~

251

300

VI

Y4rat HTCSSRVGQM KRINGMLMAM VTAPAVLWLP LHVFNTLEDW YQBAIPACHG
 Y4hum GTYSLRAGHM KQVNVVVLVVM VVAFAVLWLP LHVFNSLEDW HHEAIPICHG

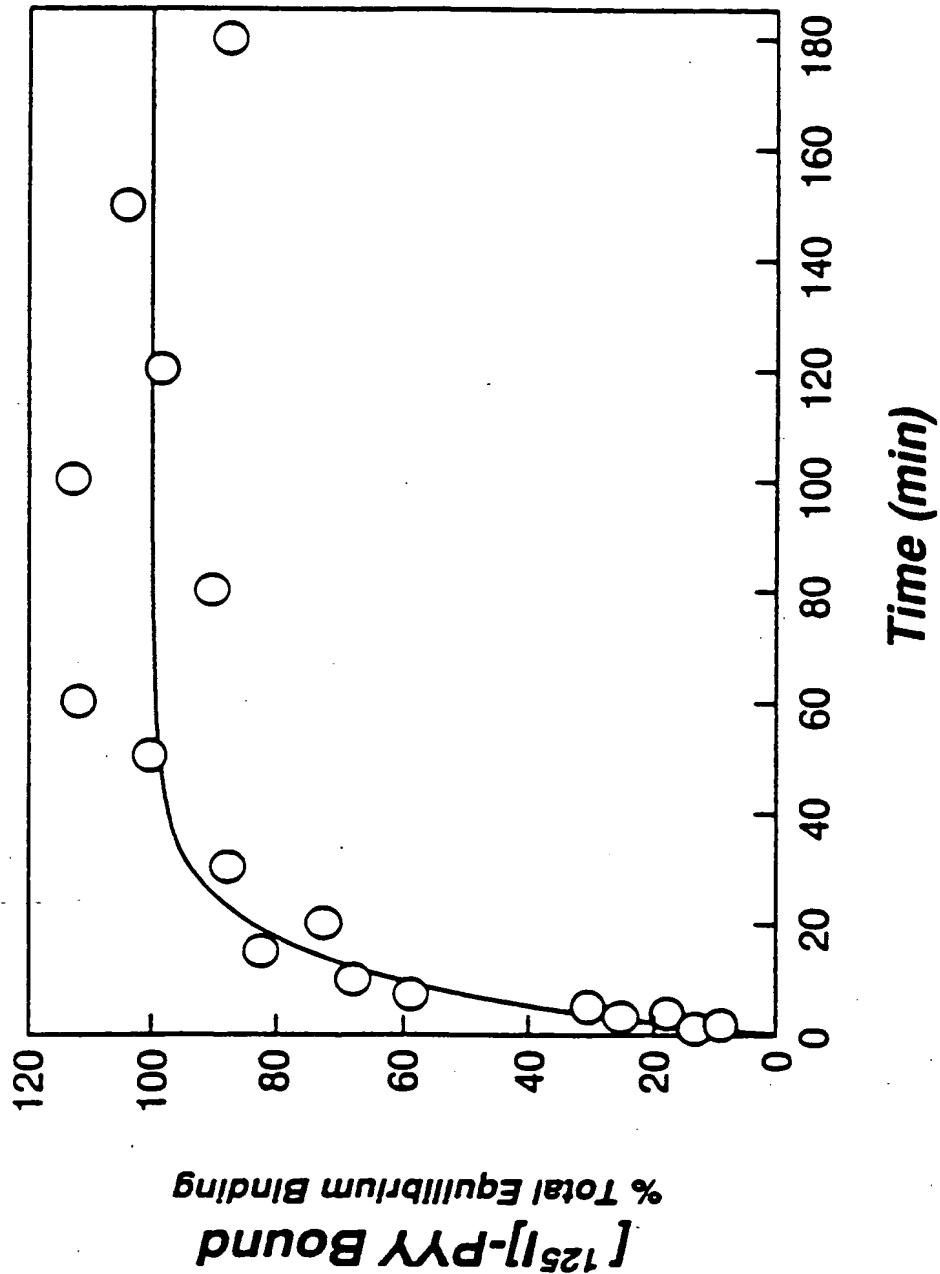
301

350

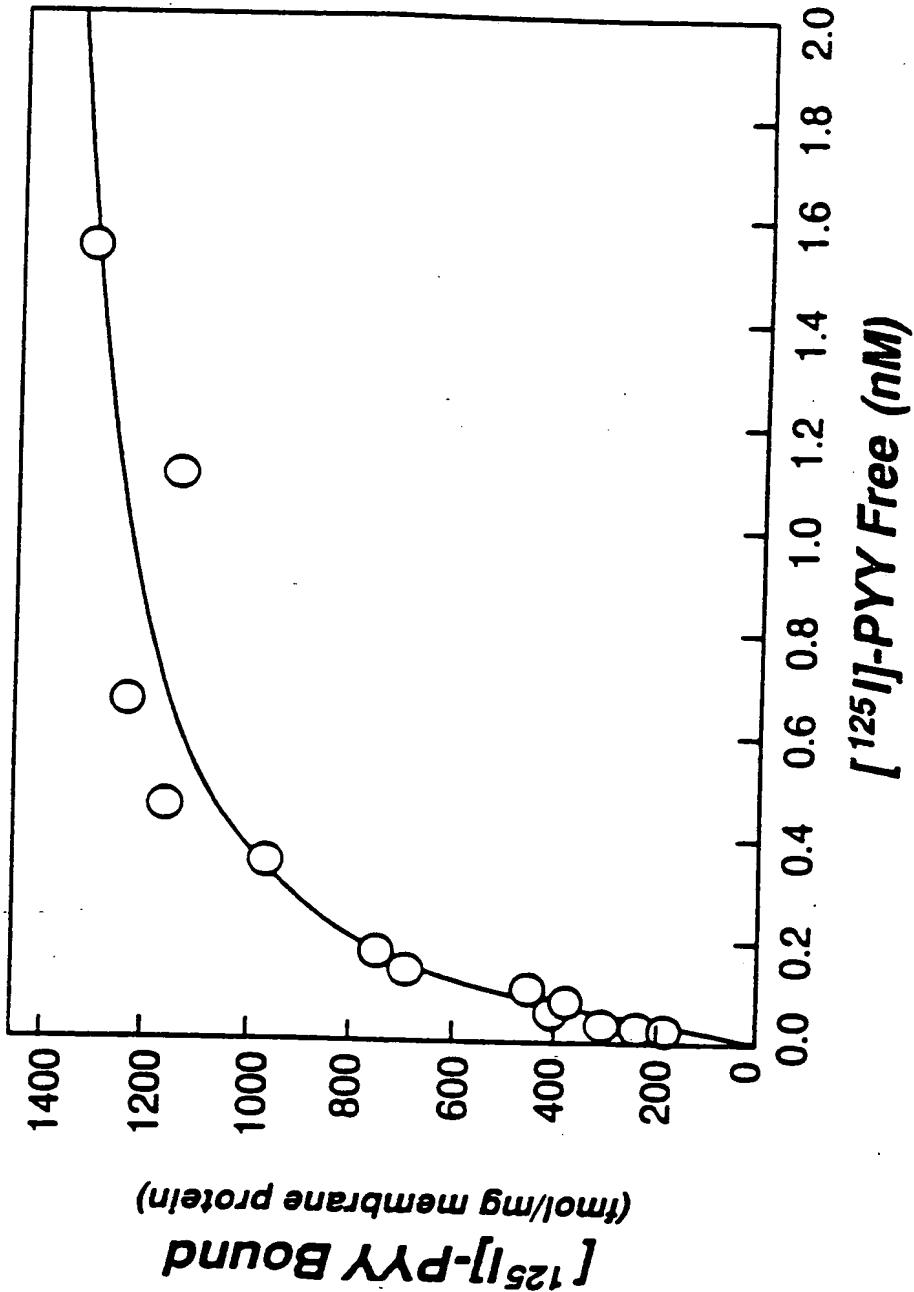
VII

Y4rat NLIFLMCHLF AMASTCVNPP IYGFLNINPK KDIKALVLTC RCRPPQGEPE
 Y4hum NLIFLVCHLL AMASTCVNPP IYGFLNTNPK KEIKALVLTC QQSAPLEESE

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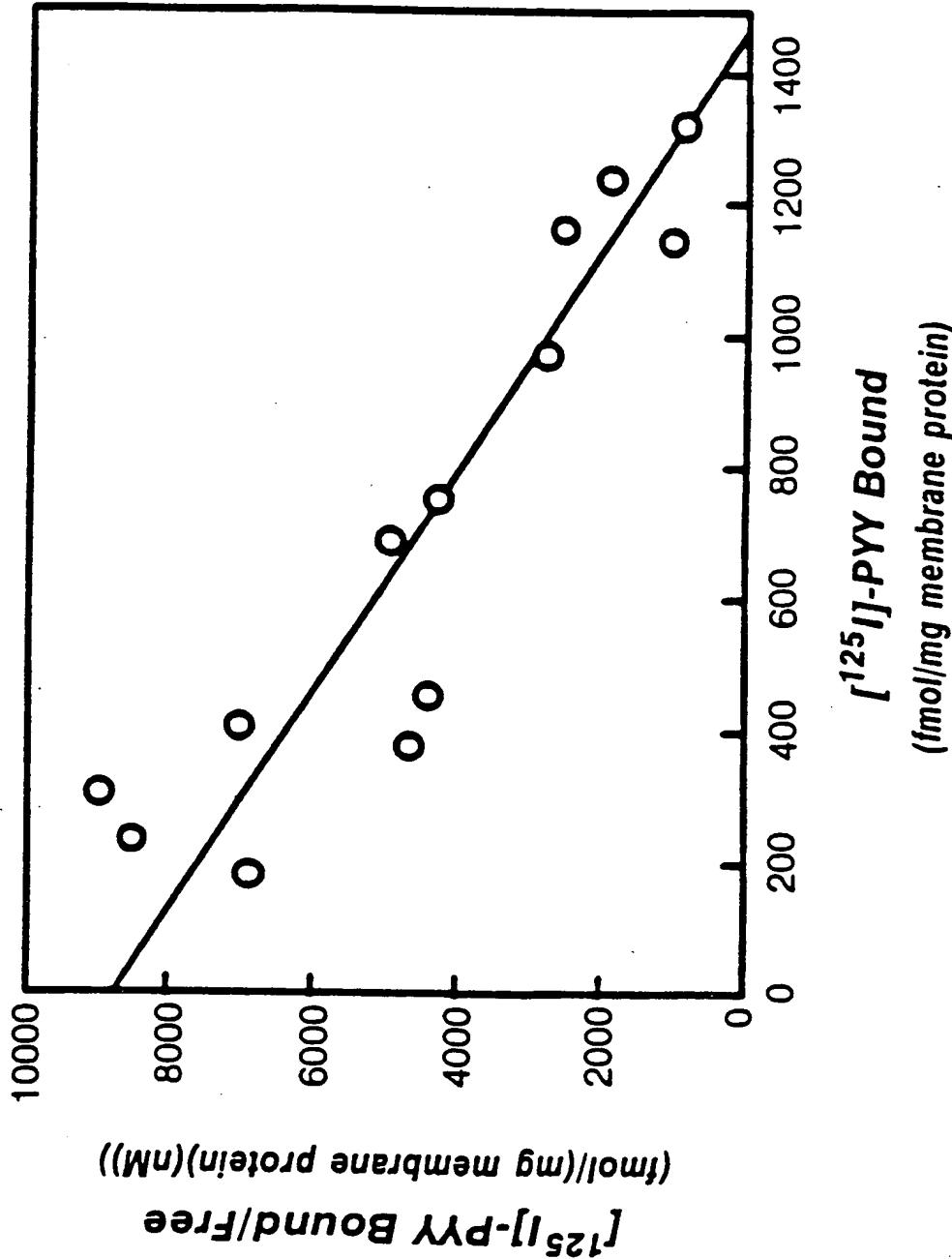
FIGURE 5

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FIGURE 6A

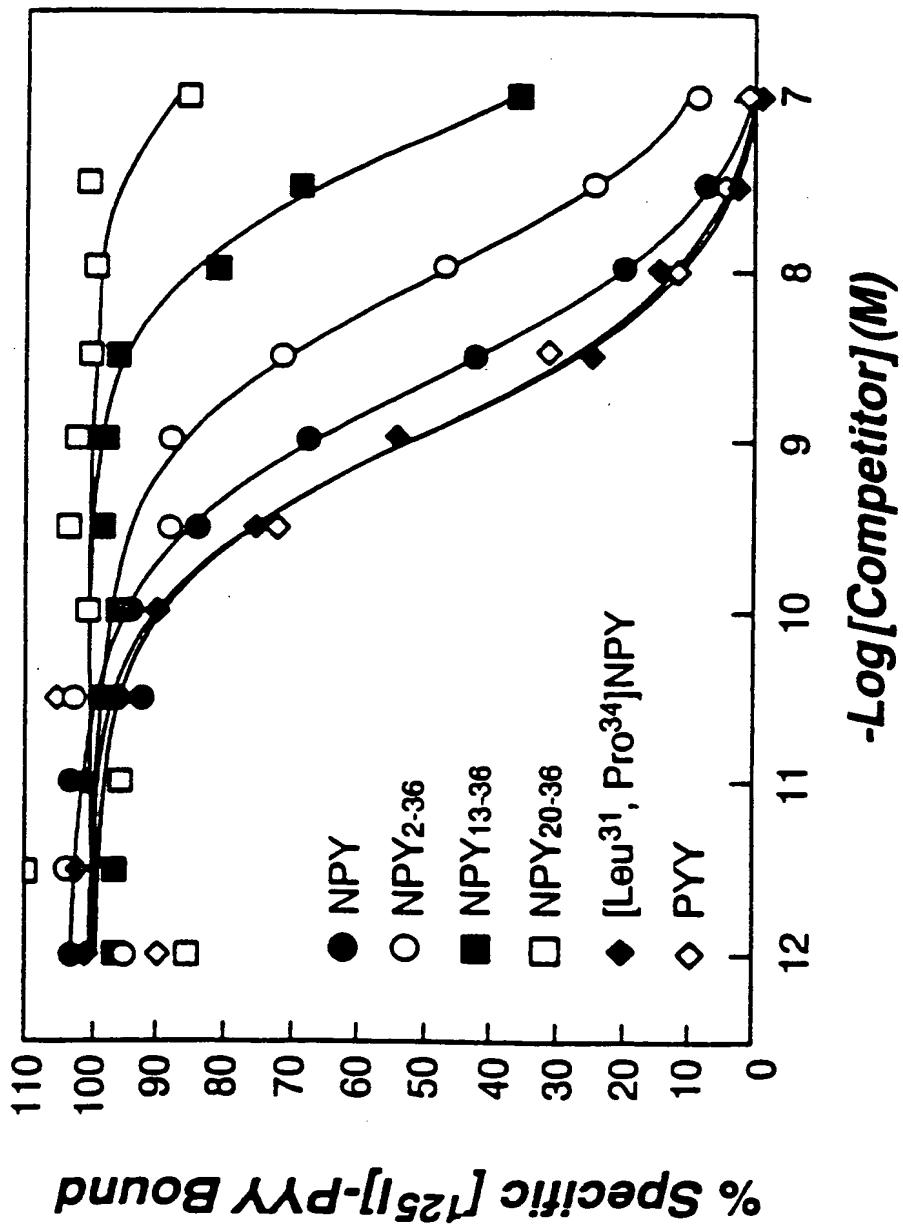
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FIGURE 6B

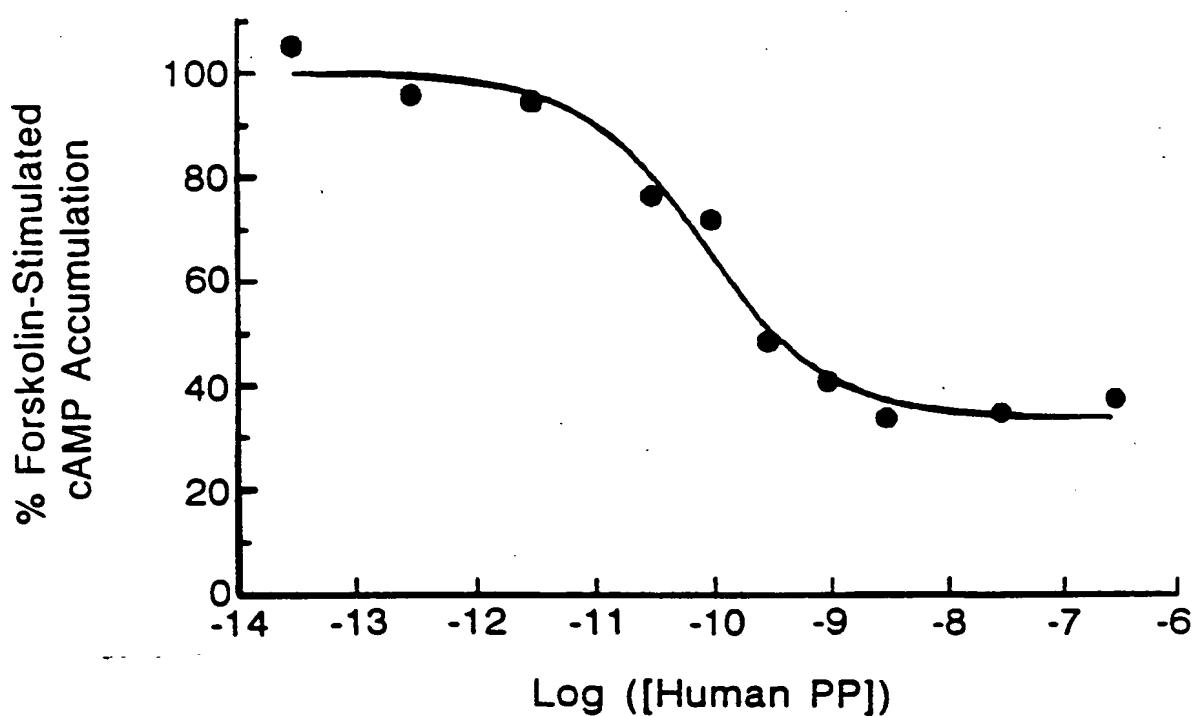


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FIGURE 7



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FIGURE 8

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FIGURE 9A

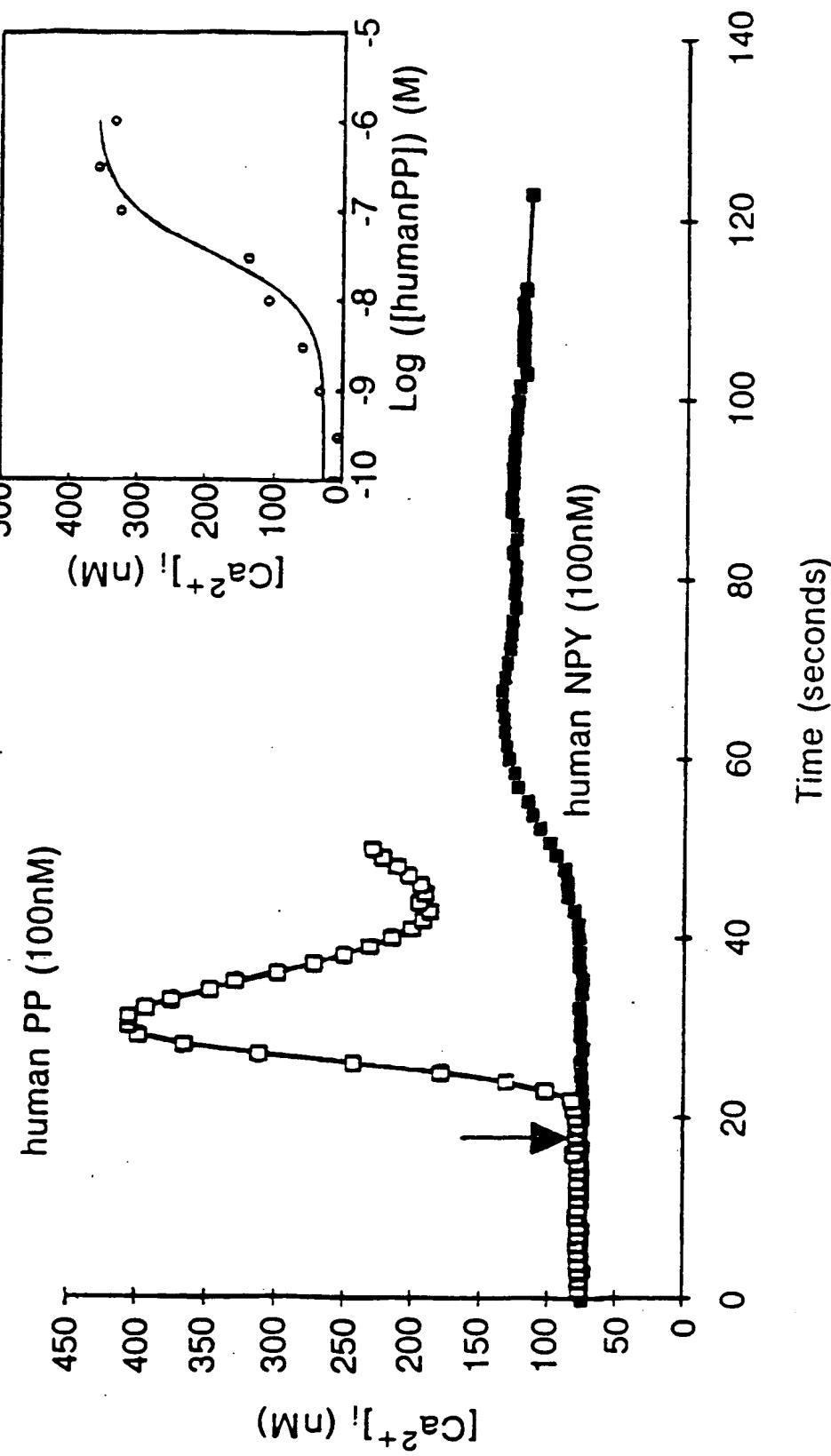
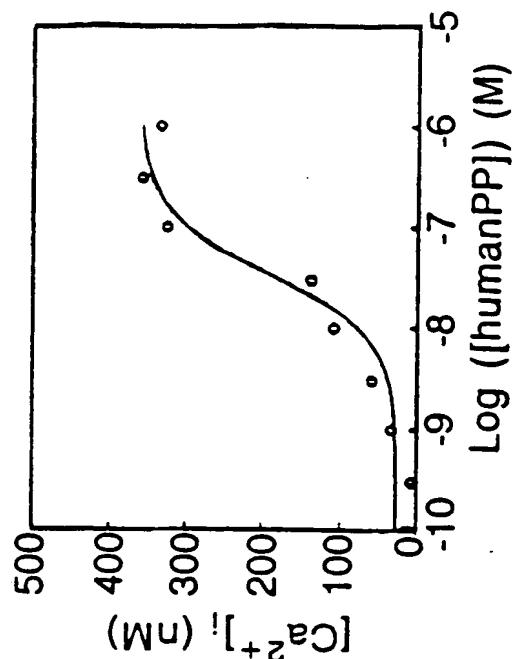


FIGURE 9B



Time (seconds)